

# SEQUENCE LISTING

<110> Scott, Fred W.

<120> Recombinant Multivalent Viral Vaccine

<130> 18617.0016

<140> 08/552,369

<141> November 3, 1995

<160> 25

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<211> 2254

<212> DNA

<213> feline panieukopenia virus

<220>

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Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly	
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ggt ggt ggt ggt tct ggg ggt gtg ggg att tct acg ggt act ttc	135
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Asn Asn Gln Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu	
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65 70 75

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Ser Glu Asn Tyr Lys Arg Val Val Val Asn Asn Met Asp Lys Thr  
80 85 90

gca gtt aaa gga aac atg gct tta gat gac act cat gta caa att 315  
Ala Val Lys Gly Asn Met Ala Leu Asp Asp Thr His Val Gln Ile  
95 100 105

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Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala Trp Gly Val Trp  
110 115 120

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Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr Met Ser Glu  
125 130 135

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140 145 150

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Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val Tyr  
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170 175 180

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Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr  
200 205 210

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215 220 225

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Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp	
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ggt caa ttt tat act att gaa aat tct gtg cca gta cac tta cta	765
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Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys	
260 265 270	
aaa cca tgt aga cta aca cat aca tgg caa aca aac aga gca ttg	855
Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu	
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Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala	
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act aac ttt ggt gat ata gga gtt caa caa gat aaa aga cgt ggt	945
Thr Asn Phe Gly Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly	
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320 325 330	
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Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe	
335 340 345	
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Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp	
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Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr	
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Asn	Leu	Pro	Val	Thr	Asn	Asp	Asn	Val	Leu	Leu	Pro	Thr	Asp	Pro		
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Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn	Asn	Val	Pro	Pro	Val	Tyr	Pro		
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Asp	Pro	Asp	Ala	Ser	Ala	Asn	Met	Ser	Arg	Ile	Val	Thr	Tyr	Ser		
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Asp	Phe	Trp	Trp	Lys	Gly	Lys	Leu	Val	Phe	Lys	Ala	Lys	Leu	Arg		
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Ala	Ser	His	Thr	Trp	Asn	Pro	Ile	Gln	Gln	Met	Ser	Ile	Asn	Val		
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104090" 10002050

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aggatttaga aggtttgtta tatgggtatac aataactgta agaaatagaa 1952

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agaacattta gatcatgggt agtagtttgt tttataaaat gtaattgtaa 2052

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gaatatgtta aggaccaaaa aaatcaataa aagacattta aaacttaatg 2152

gtctcgtata ctgtctataa ggtgaactaa ccttaccata agtatcaact 2202

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<213> rabies virus

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Pro	Leu	Cys	Phe	Gly	Lys	Phe	Pro	Ile	Tyr	Thr	Ile	Leu	Asp	
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aag	ctt	ggt	ccc	tgg	agc	ccg	att	gac	ata	cat	cac	ctc	agc	126
Lys	Leu	Gly	Pro	Trp	Ser	Pro	Ile	Asp	Ile	His	His	Leu	Ser	
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tgc	cca	aac	aat	ttg	gta	gtg	gag	gac	gaa	gga	tgc	acc	aac	168
Cys	Pro	Asn	Asn	Leu	Val	Val	Glu	Asp	Glu	Gly	Cys	Thr	Asn	
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ctg	tca	ggg	ttc	tcc	tac	atg	gaa	ctt	aaa	gtt	gga	tac	atc	210
Leu	Ser	Gly	Phe	Ser	Tyr	Met	Glu	Leu	Lys	Val	Gly	Tyr	Ile	
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Leu	Ala	Ile	Lys	Met	Asn	Gly	Phe	Thr	Cys	Thr	Gly	Val	Val	
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Thr	Thr	Phe	Lys	Arg	Lys	His	Phe	Arg	Pro	Thr	Pro	Asp	Ala	
	100					105					110			
tgt	aga	gcc	gcg	tac	aac	tgg	aag	atg	gcc	ggt	gac	ccc	aga	378
Cys	Arg	Ala	Ala	Tyr	Asn	Trp	Lys	Met	Ala	Gly	Asp	Pro	Arg	
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Tyr	Glu	Glu	Ser	Leu	His	Asn	Pro	Tyr	Pro	Asp	Tyr	Arg	Trp	
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ctt	cga	act	gta	aaa	acc	acc	aag	gag	tct	ctc	gtt	atc	ata	462
Leu	Arg	Thr	Val	Lys	Thr	Thr	Lys	Glu	Ser	Leu	Val	Ile	Ile	
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His Ser Arg Val Phe Pro Ser Gly Lys Cys Ser Gly Val Ala					
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gtg tct tct acc tac tgc tcc act aac cac gat tac acc att					588
Val Ser Ser Thr Tyr Cys Ser Thr Asn His Asp Tyr Thr Ile					
185		190		195	
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Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys Asp Ile					
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Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu					
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Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu					
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Lys Gly Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu					
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Arg Leu Met Asp Gly Thr Trp Val Ala Met Gln Thr Ser Asn					
255		260		265	
gaa acc aaa tgg tgc gct ccc gat cag ttg gtg aac ctg cac					840
Glu Thr Lys Trp Cys Pro Pro Asp Gln Leu Val Asn Leu His					
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Asp Phe Arg Ser Asp Glu Ile Glu His Leu Val Val Glu Glu					
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Leu Val Arg Lys Arg Glu Glu Cys Leu Asp Ala Leu Glu Ser					
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Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu Ser His					
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Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser	
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365 370 375	
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380 385 390	
cca gag atg caa tca tcc ctc ctc cag caa cat atg gag ttg	1218
Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu	
395 400 405	
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Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp	
410 415 420	
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Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe	
425 430	
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Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly	
435 440 445	
gtt gac ttg ggt ctc ccg aac tgg ggg aag tat gta tta ctg	1386
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450 455 460	
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Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu	
465 470 475	



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480 485 490

cac aat ctc aga ggg aca ggg agg gag gtg tca gtc act ccc 1512  
His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro  
495 500

caa agc ggg aag atc ata tct tca tgg gaa tca cac aag agt 1554  
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<212> DNA

<213> P11 late promoter and leader sequence

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<212> DNA

<213> artificial sequence

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<223> forward primer

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<212> DNA

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<220> reverse primer

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<211> 18

<212> DNA

<213> artificial sequence

<220> sequencing primer

<223>

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<212> DNA

<213> feline calicivirus

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Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val	
20 25 30	
ggc ttc tgc gat aac cct tta atg tgt tgt tat cct gaa tta cta	135
Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu	
35 40 45	
cct gaa ttt ggc acc atg tgg gat tgt gat caa tcg cca ctc caa	180
Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln	
50 55 60	
gtc tac ctt gag tca atc ctg ggt gat gat gaa tgg tcc tcc act	225
Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr	
65 70 75	
cat gaa gca att gac cca gtt gtg cca cca atg cat tgg gat gaa	270
His Glu Ala Ile Asp Pro Val Val Pro Pro Met His Trp Asp Glu	
80 85 90	
gcc gga aaa atc ttc caa cca cac cct ggc gtc ctt atg cat cac	315
Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His	
95 100 105	
ctc atc tgt aag gtt gca gaa gga tgg gac cca aac ctg cca ctt	360
Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu	
110 115 120	
ttc cgc ttg gaa gcg gac gat ggt tcc atc acg aca cct gaa cag	405
Phe Arg Leu Glu Ala Asp Asp Gly Ser Ile Thr Thr Pro Glu Gln	
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gga aca atg gtt ggt gga gtc att gct gag ccc aac gcc caa atg	450
Gly Thr Met Val Gly Gly Val Ile Ala Glu Pro Asn Ala Gln Met	
140 145 150	
tca acc gca gct gac atg gcc act ggg aaa agt gtg gac tct gag	495
Ser Thr Ala Ala Asp Met Ala Thr Gly Lys Ser Val Asp Ser Glu	

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Trp	Glu	Ala	Phe	Phe	Ser	Phe	His	Thr	Ser	Val	Asn	Trp	Ser	Thr	
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tct	gaa	act	cag	ggg	aag	ata	ctc	ttt	aaa	caa	tcc	tta	gga	cca	585
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Leu	Leu	Asn	Pro	Tyr	Leu	Thr	His	Leu	Ala	Lys	Leu	Tyr	Val	Ala	
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Trp	Ser	Gly	Ser	Val	Asp	Val	Arg	Phe	Ser	Ile	Ser	Gly	Ser	Gly	
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gtc	ttt	gga	ggg	aaa	tta	gct	gct	att	gtt	gtg	ccg	cca	gga	att	720
Val	Phe	Gly	Gly	Lys	Leu	Ala	Ala	Ile	Val	Val	Pro	Pro	Gly	Ile	
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gat	cct	gtt	caa	agt	act	tca	atg	ctg	caa	tat	cct	cat	gtc	ctc	765
Asp	Pro	Val	Gln	Ser	Thr	Ser	Met	Leu	Gln	Tyr	Pro	His	Val	Leu	
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Phe	Asp	Ala	Arg	Gln	Val	Glu	Pro	Val	Ile	Phe	Ser	Ile	Pro	Asp	
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cta	aga	agc	acc	tta	tat	cac	ctt	atg	tct	gac	act	gat	acc	aca	855
Leu	Arg	Ser	Thr	Leu	Tyr	His	Leu	Met	Ser	Asp	Thr	Asp	Thr	Thr	
				275					280					285	
tcg	ttg	gta	atc	atg	gtg	tac	aat	gat	ctt	att	aac	ccc	tat	gct	900
Ser	Leu	Val	Ile	Met	Val	Tyr	Asn	Asp	Leu	Ile	Asn	Pro	Tyr	Ala	
				290					295					300	
aat	gac	tca	aac	tct	tcg	ggc	tgc	att	gtc	act	gtg	gaa	act	aaa	945
Asn	Asp	Ser	Asn	Ser	Ser	Gly	Cys	Ile	Val	Thr	Val	Glu	Thr	Lys	
				305					310					315	
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Pro	Gly	Pro	Asp	Phe	Lys	Phe	His	Leu	Leu	Lys	Pro	Pro	Gly	Ser	
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Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser	
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tct tcg ctt tgg att gga aat cgg ttt tgg tct gac ata acc gat	1080
Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp	
350 355 360	
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Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp	
365 370 375	
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Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro	
380 385 390	
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Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile	
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gga gtg gcc acc gac tac att gtt ccc ggc ata cca gat gga tgg	1260
Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp	
410 415 420	
ccc gac aca aca atc cca ggt gag ttg gta cct gtt ggt gac tat	1305
Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr	
425 430 435	
gcc atc act aat ggc acc aac aat gat atc acc aca gct gcg cag	1350
Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln	
440 445 450	
tac gat gca gcc act gag att aga aac aac acc aat ttc aga ggc	1395
Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly	
455 460 465	
atg tac att tgt ggt tct ctt caa aga gct tgg ggg gat aag aag	1440
Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys	
470 475 480	
att tca aat act gct ttt atc aca acc ggc acg gtt gat gga gcc	1485
Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala	
485 490 495	

aaa ttg ata ccc agt aat acc att gac caa aca aaa att gcc gta	1530
Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val	
500 505 510	
ttc caa gac aca cat gcg aat aag cat gtc cag acc tcg gac gac	1575
Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp	
515 520 525	
aca ttg gcc ctg ctt ggt tat act ggt att ggt gag gaa gca att	1620
Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile	
530 535 540	
ggg gct gac cgc gat aga gtt gtg cga att agc gtc ctc ccg gaa	1665
Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu	
545 550 555	
cgt ggc gca cgt ggt ggc aat cac cca atc ttc cac aaa aac tct	1710
Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser	
560 565 570	
atc aag ctt ggt tat gta att agg tcc att gat gtg ttc aat tct	1755
Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser	
575 580 585	
caa att ctg cat acc tct agg caa ctt tcc ctc aat cat tac tta	1800
Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu	
590 595 600	
ttg tcg cct gac tcc ttt gct gtc tat agg att att gac tct aat	1845
Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn	
605 610 615	
gga tcc tgg ttt gac ata ggc att gat aat gat gga ttt tct ttt	1890
Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe	
620 625 630	
gtt ggt gta tca agt att ggt aaa tta gag ttt cct tta act gcc	1935
Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala	
635 640 645	
tcc tac atg gga att caa ttg gca aaa att cga ctt gcc tct aac	1980
Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn	
650 655 660	
att agg agt gtg atg aca aaa tta tga	2007

Ile Arg Ser Val Met Thr Lys Leu  
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<211> 582

<212> DNA

<213> artificial sequence

<220> hemagglutinin left arm

<223>

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gtaaaaataa	atcacatttt	tatactaata	tgaaacaact	atcgatagtt	150
atattgctac	tatcgatagt	atatacaacc	aaacctcatc	ctacacagat	200
atcaaaaaaa	ctaggcgatg	atgctactct	atcgtgtaat	agaaacaata	250
cacatggata	tcttgatcatg	agttcttggt	ataagaaacc	agactccatt	300
attctcttag	cagccaaaaa	cgatgtcgta	tactttgatg	attatacagc	350
ggataaagta	tcatacgatt	caccgatga	tactctagct	acaattatta	400
caattaaatc	attgacatct	gcagatgcag	gtacttatat	atgcgcattc	450
tttataacat	caacaaatga	tacggataaa	atagattatg	aagaatactt	500
catagatttg	gttgtaaata	cagctaattg	atccactatt	gacgcgattc	550
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<210> 9

<211> 447

<212> DNA

<213> artificial sequence

<220> hemagglutinin right arm

<223>

<400> 1

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atgaaccaat	atctgtatca	tcctcgatac	caacaacggt	agaaagtgtt	100
acaatatcta	ctacaaaata	tacaactagt	gactttatag	agatatttgg	150

cattgtttca	ctaattttat	tattggccgt	ggcgattttc	tgtattatat	200
tattttctgta	gtggacggtc	tcgtaaacaa	gaaacaaata	tattatagat	250
tttaactcag	ataaatgtct	ggaataatta	aatctatcgt	tttgagcgga	300
ccatctgggt	ccggcaagac	agctatagtc	aggagactct	tacaagatta	350
tggaaatata	tttggatttg	tggtatccca	taccactaga	tttcctcgtc	400
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<211> 40

<212> DNA

<213> artificial sequence

<220> primer P3

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<220> primer P1

<223>

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<210> 12

<211> 27

<212> DNA

09873861-060401



<213> artificial sequence

<220> primer F2

<223>

<400> 1

gcggtaccct ggggtaggc gatagag 27

<210> 13

<211> 20

<212> DNA

<213> artificial sequence

<220> primer P5

<223>

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atttctccgt gataggtatc 20

<210> 14

<211> 22

<212> DNA

<213> artificial sequence

<220> primer P5

<223>

<400> 1

ggcctctctg ttaacgtaat gg 22

<210> 15

<211> 22

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F04090" F03E2960

<212> DNA

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<220> primer P2

<223>

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gcgtcgaagt ttgagcatgt gc 22

<210> 16

<211> 40

<212> DNA

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<223>

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<210> 17

<211> 840

<212> DNA

<213> feline infectious peritonitis virus

<220>

<223>

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atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96



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	170		175		180	
cta ctt tca gga aat cta tat gct gaa ggt ttc aaa atg gct ggt						636
Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly						
	185		190		195	
ggt tta acc atc gag cat ttg cct aaa tac gtc atg att gct aca						681
Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr						
	200		205		210	
cct agt aga acc atc gtt tat aca tta gtt gga aaa caa tta aaa						726
Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys						
	215		220		225	
gca act act gcc aca gga tgg gct tac tac gta aaa tct aaa gct						771
Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala						
	230		235		240	
ggt gat tac tca aca gaa gca cgt act gac aat ttg agt gaa cat						816
Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His						
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aaa aga cgt ggt cgt tct aac tct cgt ggt cgg aag aat aat gat						90
Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp						

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ata cct ttg tca ttc tac aac ccc att acc ctc gaa caa gga tct	135					
Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser						
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aaa ttt tgg aat tta tgt ccg aga gac ctt gtt ccc aaa gga ata	180					
Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile						
	50		55		60	
ggg aat aag gat caa caa att ggt tat tgg aat aga cag att cgt	225					
Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg						
	65		70		75	
tat cgt att gta aaa ggc cag cgt aag gaa ctc gct gag agg tgg	270					
Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp						
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ttc ttt tac ttc tta ggt aca gga cct cat gct gat gct aaa ttc	315					
Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe						
	95		100		105	
aaa gac aag att gat gga gtc ttc tgg gtt gca agg gat ggt gcc	360					
Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala						
	110		115		120	
atg aac aag ccc aca acg ctt ggc act cgt gga acc aat aac gaa	405					
Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu						
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Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln						
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ctt gaa gtg aac cgt tct agg aac aat tca agg tct ggt tct cag	495					
Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln						
	155		160		165	
tct aga tct gtt tca aga aac aga tct caa tct aga gga aga cac	540					
Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His						
	170		175		180	
cat tcc aat aac cag aat aat aat gtt gag gat aca att gta gcc	585					
His Ser Asn Asn Gln Asn Asn Asn Val Glu Asp Thr Ile Val Ala						
	185		190		195	

gtg	ctt	gaa	aaa	tta	ggg	gtt	act	gac	aaa	caa	agg	tca	cgt	tct	630
Val	Leu	Glu	Lys	Leu	Gly	Val	Thr	Asp	Lys	Gln	Arg	Ser	Arg	Ser	
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aaa	cct	aga	gaa	cgt	agt	gat	tcc	aaa	cct	agg	gac	aca	aca	cct	675
Lys	Pro	Arg	Glu	Arg	Ser	Asp	Ser	Lys	Pro	Arg	Asp	Thr	Thr	Pro	
				215					220					225	
aag	aat	gcc	aac	aaa	cac	acc	tgg	aag	aaa	act	gca	ggc	aag	gga	720
Lys	Asn	Ala	Asn	Lys	His	Thr	Trp	Lys	Lys	Thr	Ala	Gly	Lys	Gly	
				230					235					240	
gat	gtg	aca	act	ttc	tat	ggg	gct	aga	agt	agt	tca	gct	aac	ttt	765
Asp	Val	Thr	Thr	Phe	Tyr	Gly	Ala	Arg	Ser	Ser	Ser	Ala	Asn	Phe	
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Gly	Asp	Ser	Asp	Leu	Val	Ala	Asn	Gly	Asn	Ala	Ala	Lys	Cys	Tyr	
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cct	cag	ata	gct	gaa	tgt	gtt	cca	tca	gtg	tct	agc	ata	atc	ttt	855
Pro	Gln	Ile	Ala	Glu	Cys	Val	Pro	Ser	Val	Ser	Ser	Ile	Ile	Phe	
				275					280					285	
ggc	agt	caa	tgg	tct	gct	gaa	gaa	gct	ggg	gat	caa	gtg	aaa	gtc	900
Gly	Ser	Gln	Trp	Ser	Ala	Glu	Glu	Ala	Gly	Asp	Gln	Val	Lys	Val	
				290					295					300	
acg	ctc	act	cac	acc	tac	tac	ctg	cca	aag	gat	gat	gcc	aaa	act	945
Thr	Leu	Thr	His	Thr	Tyr	Tyr	Leu	Pro	Lys	Asp	Asp	Ala	Lys	Thr	
				305					310					315	
agt	caa	ttc	cta	gaa	cag	att	gac	gct	tac	aag	cga	cct	tct	gaa	990
Ser	Gln	Phe	Leu	Glu	Gln	Ile	Asp	Ala	Tyr	Lys	Atg	Pro	Ser	Glu	
				320					325					330	
gtg	gct	aag	gat	cag	agg	caa	aga	aga	tcc	cgt	tct	aag	tct	gct	1035
Val	Ala	Lys	Asp	Gln	Arg	Gln	Arg	Arg	Ser	Arg	Ser	Lys	Ser	Ala	
				335					340					345	
gat	aag	aag	cct	gag	gag	ttg	tct	gta	act	ctt	gtg	gag	gca	tac	1080
Asp	Lys	Lys	Pro	Glu	Glu	Lys	Ser	Val	Thr	Leu	Val	Glu	Ala	Tyr	
				350					355					360	
aca	gat	gtg	ttt	gat	gac	aca	cag	gtt	gag	atg	att	gat	gag	gtt	1125

Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val  
 365 370 375

acg aac taa acgcatgctc 1144  
 Thr Asn  
 377

<210> 19

<211> 1979

<212> DNA

<213> feline leukemia virus

<220>

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<400> 1

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 Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu  
 1 5 10 15

tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac 140  
 Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp  
 20 25 30

ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act 185  
 Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr  
 35 40 45

tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc 230  
 Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr  
 50 55 60

tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt 275  
 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val  
 65 70 75

gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta 320  
 Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu

00673881 060401  
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	80	85	90	
aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa	365			
Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys				
	95	100	105	
tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac	410			
Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr				
	110	115	120	
ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag	455			
Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys				
	125	130	135	
gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg	500			
Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp				
	140	145	150	
gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca	545			
Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser				
	155	160	165	
tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc	590			
Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser				
	170	175	180	
tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag	635			
Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys				
	185	190	195	
gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga	680			
Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg				
	200	205	210	
cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc	725			
Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser				
	215	220	225	
cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac	770			
Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn				
	230	235	240	
cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca	815			
Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr				



				245					250					255				
ggg	tcc	aaa	gtg	gcg	acc	cag	agg	ccc	caa	acg	aat	gaa	agc	gcc	860			
Gly	Ser	Lys	Val	Ala	Thr	Gln	Arg	Pro	Gln	Thr	Asn	Glu	Ser	Ala				
				260					265					270				
cca	agg	tct	gtt	gcc	ccc	acc	acc	atg	ggt	ccc	aaa	cgg	att	ggg	905			
Pro	Arg	Ser	Val	Ala	Pro	Thr	Thr	Met	Gly	Pro	Lys	Arg	Ile	Gly				
				275					280					285				
acc	gga	gat	agg	tta	ata	aat	tta	gta	caa	ggg	aca	tac	cta	gcc	950			
Thr	Gly	Asp	Arg	Leu	Ile	Asn	Leu	Val	Gln	Gly	Thr	Tyr	Leu	Ala				
				290					295					300				
tta	aat	gcc	acc	gac	ccc	aac	aaa	act	aaa	gac	tgt	tgg	ctc	tgc	995			
Leu	Asn	Ala	Thr	Asp	Pro	Asn	Lys	Thr	Lys	Asp	Cys	Trp	Leu	Cys				
				305					310					315				
ctg	gtt	tct	cga	cca	ccc	tat	tac	gaa	ggg	att	gca	atc	tta	ggt	1040			
Leu	Val	Ser	Arg	Pro	Pro	Tyr	Tyr	Glu	Gly	Ile	Ala	Ile	Leu	Gly				
				320					325					330				
acc	tac	agc	aac	caa	aca	aac	ccc	ccc	cca	tcc	tgc	cta	tct	act	1085			
Asn	Tyr	Ser	Asn	Gln	Thr	Asn	Pro	Pro	Pro	Ser	Cys	Leu	Ser	Ile				
				335					340					345				
ccg	caa	cac	aaa	cta	act	ata	tct	gaa	gta	tca	ggg	caa	gga	atg	1130			
Pro	Gln	His	Lys	Leu	Thr	Ile	Ser	Glu	Val	Ser	Gly	Gln	Gly	Met				
				350					355					360				
tgc	ata	ggg	act	gtt	cct	aaa	acc	cac	cag	gct	ttg	tgc	aat	aag	1175			
Cys	Ile	Gly	Thr	Val	Pro	Lys	Thr	His	Gln	Ala	Leu	Cys	Asn	Lys				
				365					370					375				
aca	caa	cag	gga	cat	aca	ggg	gcg	cac	tat	cta	gcc	gcc	ccc	aac	1220			
Thr	Gln	Gln	Gly	His	Thr	Gly	Ala	His	Tyr	Leu	Ala	Ala	Pro	Asn				
				380					385					390				
ggc	acc	tat	tgg	gcc	tgt	aac	act	gga	ctc	acc	cca	tgc	att	tcc	1265			
Gly	Thr	Tyr	Trp	Ala	Cys	Asn	Thr	Gly	Leu	Thr	Pro	Cys	Ile	Ser				
				395					400					405				

atg gcg gtg ctc aat tgg acc tct gat ttt tgt gtc tta atc gaa 1310  
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410 415 420

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425 430 435

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His Phe Ala Lys Ala Val Arg Phe Arg Axx Glu Pro Ile Ser Leu  
440 445 450

acg gtt gcc ctt atg ttg gga gga ctt act gta ggg ggc ata gcc 1445  
Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala  
455 460 465

gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag 1490  
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470 475 480

ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta 1535  
Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu  
485 490 495

gaa gaa tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct 1580  
Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser  
500 505 510

gaa gta gtc tta caa aac aga cgg ggc cta gat att cta ttc tta 1625  
Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu  
515 520 525

caa gag gga ggg ctc tgt gcc gca ttg aaa gaa gaa tgt tgc ttc 1670  
Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe  
530 535 540

tat gcg gat cac acc gga ctc gtc cga gac aat atg gcc aaa tta 1715  
Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu  
545 550 555

aga gaa aga cta aaa cag cgg caa caa ctg ttt gac tcc caa cag 1760  
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560 565 570

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575 580 585

cta att tcc tcc att atg ggc ccc tta cta atc cta ctc cta att 1850  
Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Leu Ile  
590 595 600

ctc ctc ttc ggc cca tgc atc ctt aac cga tta gta caa ttc gta  
1895 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe  
Val  
605 610 615

aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag  
1940 Lys Asp Axa Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln  
Gln  
620 625 630

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635 640

<210> 20

<211> 584

<212> PRT

<213> feline panleukopenia peritonitis virus

<220>

<223>

<400> 1

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Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly  
20 25 30

Gly Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe  
35 40 45

Asn	Asn	Gln	Thr	Glu	Phe	Lys	Phe	Leu	Glu	Asn	Gly	Trp	Val	Glu	
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Ile	Thr	Ala	Asn	Ser	Ser	Arg	Leu	Val	His	Leu	Asn	Met	Pro	Glu	
				65					70					75	
Ser	Glu	Asn	Tyr	Lys	Arg	Val	Val	Val	Asn	Asn	Met	Asp	Lys	Thr	
				80					85					90	
Ala	Val	Lys	Gly	Asn	Met	Ala	Leu	Asp	Asp	Thr	His	Val	Gln	Ile	
				95					100					105	
Val	Thr	Pro	Trp	Ser	Leu	Val	Asp	Ala	Asn	Ala	Trp	Gly	Val	Trp	
				110					115					120	
Phe	Asn	Pro	Gly	Asp	Trp	Gln	Leu	Ile	Val	Asn	Thr	Met	Ser	Glu	
				125					130					135	
Leu	His	Leu	Val	Ser	Phe	Glu	Gln	Glu	Ile	Phe	Asn	Val	Val	Leu	
				140					145					150	
Lys	Thr	Val	Ser	Glu	Ser	Ala	Thr	Gln	Pro	Pro	Thr	Lys	Val	Tyr	
				155					160					165	
Asn	Asn	Asp	Leu	Thr	Ala	Ser	Leu	Met	Val	Ala	Leu	Asp	Ser	Asn	
				170					175					180	
Asn	Thr	Met	Pro	Phe	Thr	Pro	Ala	Ala	Met	Arg	Ser	Glu	Thr	Leu	
				185					190					195	
Gly	Phe	Tyr	Pro	Trp	Lys	Pro	Thr	Ile	Pro	Thr	Pro	Trp	Arg	Tyr	
				200					205					210	
Tyr	Phe	Gln	Trp	Asp	Arg	Thr	Leu	Ile	Pro	Ser	His	Thr	Gly	Thr	
				215					220					225	
Ser	Gly	Thr	Pro	Thr	Asn	Ile	Tyr	His	Gly	Thr	Asp	Pro	Asp	Asp	
				230					235					240	
Val	Gln	Phe	Tyr	Thr	Ile	Glu	Asn	Ser	Val	Pro	Val	His	Leu	Leu	
				245					250					255	
Arg	Thr	Gly	Asp	Glu	Phe	Ala	Thr	Gly	Thr	Phe	Phe	Phe	Asp	Cys	
				260					265					270	

Lys	Pro	Cys	Arg	Leu	Thr	His	Thr	Trp	Gln	Thr	Asn	Axg	Ala	Leu	275	280	285
Gly	Leu	Pro	Pro	Phe	Leu	Asn	Ser	Leu	Pro	Gln	Ser	Glu	Gly	Ala	290	295	300
Thr	Asn	Phe	Gly	Asp	Ile	Gly	Val	Gln	Gln	Asp	Lys	Arg	Arg	Gly	305	310	315
Val	Thr	Gln	Met	Gly	Asn	Thr	Asp	Tyr	Ile	Thr	Glu	Ala	Thr	Ile	320	325	330
Met	Arg	Pro	Ala	Glu	Val	Gly	Tyr	Ser	Ala	Pro	Tyr	Tyr	Ser	Phe	335	340	345
Glu	Ala	Ser	Thr	Gln	Gly	Pro	Phe	Lys	Ile	Pro	Ile	Ala	Ala	Gly	350	355	360
Arg	Gly	Gly	Ala	Gln	Thr	Asp	Glu	Asn	Gln	Ala	Ala	Asp	Gly	Asp	365	370	375
Pro	Arg	Tyr	Ala	Phe	Gly	Arg	Gln	His	Gly	Gln	Lys	Thr	Thr	Thr	380	385	390
Thr	Gly	Glu	Thr	Pro	Glu	Arg	Phe	Thr	Tyr	Ile	Ala	His	Gln	Asp	395	400	405
Thr	Gly	Arg	Tyr	Pro	Ala	Gly	Asp	Trp	Ile	Gln	Asn	Ile	Asn	Phe	410	415	420
Asn	Leu	Pro	Val	Thr	Asn	Asp	Asn	Val	Leu	Leu	Pro	Thr	Asp	Pro	425	430	435
Ile	Gly	Gly	Lys	Thr	Gly	Ile	Asn	Tyr	Thr	Asn	Ile	Phe	Asn	Thr	440	445	450
Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn	Asn	Val	Pro	Pro	Val	Tyr	Pro	455	460	465
Asn	Gly	Gln	Ile	Trp	Asp	Lys	Glu	Phe	Asp	Thr	Asp	Leu	Lys	Pro	470	475	480

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T01090" T88E7860

Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro  
485 490 495

Gly Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr  
500 505 510

Asp Pro Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser  
515 520 525

Asp Phe Trp Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg  
530 535 540

Ala Ser His Thr Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val  
545 550 555

Asp Asn Gln Phe Asn Tyr Leu Pro Asn Asn Ile Gly Ala Met Lys  
560 565 570

Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg Lys Leu Tyr  
575 580

<210> 21

<211> 524

<212> PRT

<213> rabies virus

<220>

<223>

<400> 1

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe  
1 5 10

Pro Leu Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp  
15 20 25

Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser  
30 35 40

09873881-060401  
"04090" F88E2850

Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn  
45 50 55

Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile  
60 65 70

Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val  
75 80

Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr  
85 90 95

Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala  
100 105 110

Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg  
115 120 125

Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp  
130 135 140

Leu Arg Thr Val Lys Thr Thr Lys Glu Ser Leu Val Ile Ile  
145 150

Ser Pro Ser Val Ala Asp Leu Asp Pro Tyr Asp Arg Ser Leu  
155 160 165

His Ser Arg Val Phe Pro Ser Gly Lys Cys Ser Gly Val Ala  
170 175 180

Val Ser Ser Thr Tyr Cys Ser Thr Asn His Asp Tyr Thr Ile  
185 190 195

Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys Asp Ile  
200 205 210

Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu  
215 220

Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu  
225 230 235

Lys Gly Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu  
240 245 250

Arg Leu Met Asp Gly Thr Trp Val Ala Met Gln Thr Ser Asn  
255 260 265

Glu Thr Lys Trp Cys Pro Pro Asp Gln Leu Val Asn Leu His  
270 275 280

Asp Phe Arg Ser Asp Glu Ile Glu His Leu Val Val Glu Glu  
285 290

Leu Val Arg Lys Arg Glu Glu Cys Leu Asp Ala Leu Glu Ser  
295 300 305

Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu Ser His  
310 315 320

Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile  
325 330 335

Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser  
340 345 350

Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu  
355 360

Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe  
365 370 375

Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile  
380 385 390

Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu  
395 400 405

Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp  
410 415 420

Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe  
425 430

Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly  
435 440 445

Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu  
450 455 460

09373831.060401



Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu  
 465 470 475

Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln  
 480 485 490

His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro  
 495 500

Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser  
 505 510 515

Gly Gly Glu Thr Arg Leu  
 520 524

<210> 22

<211> 668

<212> PRT

<213> feline calicivirus

<220>

<223>

<400> 1

Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp  
 1 5 10 15

Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val  
 20 25 30

Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu  
 35 40 45

Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln  
 50 55 60

Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr  
 65 70 75

05073831.050401

His	Glu	Ala	Ile	Asp	Pro	Val	Val	Pro	Pro	Met	His	Trp	Asp	Glu	80	85	90
Ala	Gly	Lys	Ile	Phe	Gln	Pro	His	Pro	Gly	Val	Leu	Met	His	His	95	100	105
Leu	Ile	Cys	Lys	Val	Ala	Glu	Gly	Trp	Asp	Pro	Asn	Leu	Pro	Leu	110	115	120
Phe	Arg	Leu	Glu	Ala	Asp	Asp	Gly	Ser	Ile	Thr	Thr	Pro	Glu	Gln	125	130	135
Gly	Thr	Met	Val	Gly	Gly	Val	Ile	Ala	Glu	Pro	Asn	Ala	Gln	Met	140	145	150
Ser	Thr	Ala	Ala	Asp	Met	Ala	Thr	Gly	Lys	Ser	Val	Asp	Ser	Glu	155	160	165
Trp	Glu	Ala	Phe	Phe	Ser	Phe	His	Thr	Ser	Val	Asn	Trp	Ser	Thr	170	175	180
Ser	Glu	Thr	Gln	Gly	Lys	Ile	Leu	Phe	Lys	Gln	Ser	Leu	Gly	Pro	185	190	195
Leu	Leu	Asn	Pro	Tyr	Leu	Thr	His	Leu	Ala	Lys	Leu	Tyr	Val	Ala	200	205	210
Trp	Ser	Gly	Ser	Val	Asp	Val	Arg	Phe	Ser	Ile	Ser	Gly	Ser	Gly	215	220	225
Val	Phe	Gly	Gly	Lys	Leu	Ala	Ala	Ile	Val	Val	Pro	Pro	Gly	Ile	230	235	240
Asp	Pro	Val	Gln	Ser	Thr	Ser	Met	Leu	Gln	Tyr	Pro	His	Val	Leu	245	250	255
Phe	Asp	Ala	Arg	Gln	Val	Glu	Pro	Val	Ile	Phe	Ser	Ile	Pro	Asp	260	265	270
Leu	Arg	Ser	Thr	Leu	Tyr	His	Leu	Met	Ser	Asp	Thr	Asp	Thr	Thr	275	280	285
Ser	Leu	Val	Ile	Met	Val	Tyr	Asn	Asp	Leu	Ile	Asn	Pro	Tyr	Ala	290	295	300

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09373881.050401

Asn	Asp	Ser	Asn	Ser	Ser	Gly	Cys	Ile	Val	Thr	Val	Glu	Thr	Lys	305	310	315
Pro	Gly	Pro	Asp	Phe	Lys	Phe	His	Leu	Leu	Lys	Pro	Pro	Gly	Ser	320	325	330
Met	Leu	Thr	His	Gly	Ser	Ile	Pro	Ser	Asp	Leu	Ile	Pro	Lys	Ser	335	340	345
Ser	Ser	Leu	Trp	Ile	Gly	Asn	Arg	Phe	Trp	Ser	Asp	Ile	Thr	Asp	350	355	360
Phe	Val	Ile	Arg	Pro	Phe	Val	Phe	Gln	Ala	Asn	Arg	His	Phe	Asp	365	370	375
Phe	Asn	Gln	Glu	Thr	Ala	Gly	Trp	Ser	Thr	Pro	Arg	Phe	Arg	Pro	380	385	390
Ile	Thr	Ile	Thr	Ile	Ser	Val	Lys	Glu	Ser	Ala	Lys	Leu	Gly	Ile	395	400	405
Gly	Val	Ala	Thr	Asp	Tyr	Ile	Val	Pro	Gly	Ile	Pro	Asp	Gly	Trp	410	415	420
Pro	Asp	Thr	Thr	Ile	Pro	Gly	Glu	Leu	Val	Pro	Val	Gly	Asp	Tyr	425	430	435
Ala	Ile	Thr	Asn	Gly	Thr	Asn	Asn	Asp	Ile	Thr	Thr	Ala	Ala	Gln	440	445	450
Tyr	Asp	Ala	Ala	Thr	Glu	Ile	Arg	Asn	Asn	Thr	Asn	Phe	Arg	Gly	455	460	465
Met	Tyr	Ile	Cys	Gly	Ser	Leu	Gln	Arg	Ala	Trp	Gly	Asp	Lys	Lys	470	475	480
Ile	Ser	Asn	Thr	Ala	Phe	Ile	Thr	Thr	Gly	Thr	Val	Asp	Gly	Ala	485	490	495
Lys	Leu	Ile	Pro	Ser	Asn	Thr	Ile	Asp	Gln	Thr	Lys	Ile	Ala	Val	500	505	510
Phe	Gln	Asp	Thr	His	Ala	Asn	Lys	His	Val	Gln	Thr	Ser	Asp	Asp	515	520	525

Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile  
 530 535 540  
 Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu  
 545 550 555  
 Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser  
 560 565 570  
 Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser  
 575 580 585  
 Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu  
 590 595 600  
 Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn  
 605 610 615  
 Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe  
 620 625 630  
 Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala  
 635 640 645  
 Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn  
 650 655 660  
 Ile Arg Ser Val Met Thr Lys Leu  
 665

<210> 23

<211> 262

<212> PRT

<213> feline infectious peritonitis virus

<220>

<223>

<400> 1

Met Lys Tyr Ile Leu Leu Ile Leu Ala Cys Ile Ile Ala Cys Val

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1		5		10		15									
Tyr	Gly	Glu	Arg	Tyr	Cys	Ala	Met	Gln	Asp	Ser	Gly	Leu	Gln	Cys	
				20					25					30	
Ile	Gln	Gly	Thr	Gln	Ser	Arg	Cys	Gln	Thr	Cys	Phe	Glu	Arg	Gly	
				35					40					45	
Asp	Leu	Ile	Trp	His	Leu	Ala	Asn	Trp	Asn	Phe	Ser	Trp	Ser	Val	
				50					55					60	
Ile	Leu	Ile	Val	Phe	Ile	Thr	Val	Leu	Gln	Tyr	Gly	Arg	Pro	Gln	
				65					70					75	
Phe	Ser	Trp	Leu	Val	Tyr	Gly	Ile	Lys	Met	Leu	Ile	Met	Trp	Leu	
				80					85					90	
Leu	Trp	Pro	Ile	Val	Leu	Ala	Leu	Thr	Ile	Phe	Asn	Ala	Tyr	Ser	
				95					100					105	
Glu	Tyr	Gln	Val	Ser	Arg	Tyr	Val	Met	Phe	Gly	Phe	Ser	Val	Ala	
				110					115					120	
Gly	Ala	Val	Val	Thr	Phe	Ala	Leu	Trp	Met	Met	Tyr	Phe	Val	Arg	
				125						130				135	
Ser	Val	Gln	Leu	Tyr	Arg	Axg	Thr	Lys	Ser	Trp	Trp	Ser	Phe	Asn	
				140					145					150	
Pro	Glu	Thr	Asn	Ala	Ile	Leu	Cys	Val	Asn	Ala	Leu	Gly	Arg	Ser	
				155					160					165	
Tyr	Val	Leu	Pro	Leu	Asp	Gly	Thr	Pro	Thr	Gly	Val	Thr	Leu	Thr	
				170					175					180	
Leu	Leu	Ser	Gly	Asn	Leu	Tyr	Ala	Glu	Gly	Phe	Lys	Met	Ala	Gly	
				185					190					195	
Gly	Leu	Thr	Ile	Glu	His	Leu	Pro	Lys	Tyr	Val	Met	Ile	Ala	Thr	
				200					205					210	
Pro	Ser	Arg	Thr	Ile	Val	Tyr	Thr	Ile	Val	Gly	Lys	Gln	Leu	Lys	
				215					220					225	
Ala	Thr	Thr	Ala	Thr	Gly	Trp	Ala	Tyr	Tyr	Val	Lys	Ser	Lys	Ala	

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T04090" T88E/860

	230		235		240
Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His					
	245		250		255
Glu Lys Leu Leu His Met Val					
	260				
<210> 24					
<211> 377					
<212> PRT					
<213> feline infectious peritonitis virus					
<220>					
<223>					
<400> 1					
Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser					
1	5		10		15
Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp					
	20		25		30
Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser					
	35		40		45
Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile					
	50		55		60
Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg					
	65		70		75
Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp					
	80		85		90

Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe  
95 100 105

Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala  
110 115 120

Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu  
125 130 135

Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln  
140 145 150

Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln  
155 160 165

Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His  
170 175 180

His Ser Asn Asn Gln Asn Asn Asn Val Glu Asp Thr Ile Val Ala  
185 190 195

Val Leu Glu Lys Leu Gly Val Thr Asp Lys Gln Arg Ser Arg Ser  
200 205 210

Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro  
215 220 225

Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly  
230 235 240

Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe  
245 250 255

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Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr  
 260 265 270

Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe  
 275 280 285

Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val  
 290 295 300

Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr  
 305 310 315

Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys Atg Pro Ser Glu  
 320 325 330

Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala  
 335 340 345

Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr  
 350 355 360

Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val  
 365 370 375

Thr Asn  
 377

<210> 25

<211> 642

<212> PRT

<213> feline leukemia virus

<220>

09073881.060401



<223>

<400> 1

Met	Glu	Ser	Pro	Thr	His	Pro	Lys	Pro	Ser	Lys	Asp	Lys	Thr	Leu	
1				5					10					15	
Ser	Trp	Asn	Leu	Ala	Phe	Leu	Val	Gly	Ile	Leu	Phe	Thr	Ile	Asp	
			20					25						30	
Ile	Gly	Met	Ala	Asn	Pro	Ser	Pro	His	Gln	Ile	Tyr	Asn	Val	Thr	
			35					40						45	
Trp	Val	Ile	Thr	Asn	Val	Gln	Thr	Asn	Thr	Gln	Ala	Asn	Ala	Thr	
			50					55						60	
Ser	Met	Leu	Gly	Thr	Leu	Thr	Asp	Ala	Tyr	Pro	Thr	Leu	His	Val	
			65					70						75	
Asp	Leu	Cys	Asp	Leu	Val	Gly	Asp	Thr	Trp	Glu	Pro	Ile	Val	Leu	
			80					85						90	
Asn	Pro	Thr	Asn	Val	Lys	His	Gly	Ala	Arg	Tyr	Ser	Ser	Ser	Lys	
			95					100						105	
Tyr	Gly	Cys	Lys	Thr	Thr	Asp	Arg	Lys	Lys	Gln	Gln	Gln	Thr	Tyr	
			110					115						120	
Pro	Phe	Tyr	Val	Cys	Pro	Gly	His	Ala	Pro	Ser	Leu	Gly	Pro	Lys	
			125					130						135	
Gly	Thr	His	Cys	Gly	Gly	Ala	Gln	Asp	Gly	Phe	Cys	Ala	Ala	Trp	
			140					145						150	
Gly	Cys	Glu	Thr	Thr	Gly	Glu	Thr	Trp	Trp	Lys	Pro	Thr	Ser	Ser	
			155					160						165	
Trp	Asp	Tyr	Ile	Thr	Val	Lys	Arg	Gly	Ser	Ser	Gln	Asp	Asn	Ser	
			170					175						180	
Cys	Glu	Gly	Lys	Cys	Asn	Pro	Leu	Val	Leu	Gln	Phe	Thr	Gln	Lys	
			185					190						195	
Gly	Arg	Gln	Ala	Ser	Trp	Asp	Gly	Pro	Lys	Met	Trp	Gly	Leu	Arg	
			200					205						210	

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Leu	Tyr	Arg	Thr	Gly	Tyr	Asp	Pro	Ile	Ala	Leu	Phe	Thr	Val	Ser	215	220	225
Arg	Gln	Val	Ser	Thr	Ile	Thr	Pro	Pro	Gln	Ala	Met	Gly	Pro	Asn	230	235	240
Leu	Val	Leu	Pro	Asp	Gln	Lys	Pro	Pro	Ser	Arg	Gln	Ser	Gln	Thr	245	250	255
Gly	Ser	Lys	Val	Ala	Thr	Gln	Arg	Pro	Gln	Thr	Asn	Glu	Ser	Ala	260	265	270
Pro	Arg	Ser	Val	Ala	Pro	Thr	Thr	Met	Gly	Pro	Lys	Arg	Ile	Gly	275	280	285
Thr	Gly	Asp	Arg	Leu	Ile	Asn	Leu	Val	Gln	Gly	Thr	Tyr	Leu	Ala	290	295	300
Leu	Asn	Ala	Thr	Asp	Pro	Asn	Lys	Thr	Lys	Asp	Cys	Trp	Leu	Cys	305	310	315
Leu	Val	Ser	Arg	Pro	Pro	Tyr	Tyr	Glu	Gly	Ile	Ala	Ile	Leu	Gly	320	325	330
Asn	Tyr	Ser	Asn	Gln	Thr	Asn	Pro	Pro	Pro	Ser	Cys	Leu	Ser	Ile	335	340	345
Pro	Gln	His	Lys	Leu	Thr	Ile	Ser	Glu	Val	Ser	Gly	Gln	Gly	Met	350	355	360
Cys	Ile	Gly	Thr	Val	Pro	Lys	Thr	His	Gln	Ala	Leu	Cys	Asn	Lys	365	370	375
Thr	Gln	Gln	Gly	His	Thr	Gly	Ala	His	Tyr	Leu	Ala	Ala	Pro	Asn	380	385	390
Gly	Thr	Tyr	Trp	Ala	Cys	Asn	Thr	Gly	Leu	Thr	Pro	Cys	Ile	Ser	395	400	405
Met	Ala	Val	Leu	Asn	Trp	Thr	Ser	Asp	Phe	Cys	Val	Leu	Ile	Glu	410	415	420
Leu	Trp	Pro	Arg	Val	Thr	Tyr	His	Gln	Pro	Glu	Tyr	Val	Tyr	Thr	425	430	435

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His	Phe	Ala	Lys	Ala	Val	Arg	Phe	Arg	Axg	Glu	Pro	Ile	Ser	Leu	440	445	450
Thr	Val	Ala	Leu	Met	Leu	Gly	Gly	Leu	Thr	Val	Gly	Gly	Ile	Ala	455	460	465
Ala	Gly	Val	Gly	Thr	Gly	Thr	Lys	Ala	Leu	Leu	Glu	Thr	Ala	Gln	470	475	480
Phe	Arg	Gln	Leu	Gln	Met	Ala	Met	His	Thr	Asp	Ile	Gln	Ala	Leu	485	490	495
Glu	Glu	Ser	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Leu	Thr	Ser	Leu	Ser	500	505	510
Glu	Val	Val	Leu	Gln	Asn	Arg	Arg	Glu	Leu	Asp	Ile	Leu	Phe	Leu	515	520	525
Gln	Glu	Gly	Gly	Leu	Cys	Ala	Ala	Leu	Lys	Glu	Glu	Cys	Cys	Phe	530	535	540
Tyr	Ala	Asp	His	Thr	Gly	Leu	Val	Arg	Asp	Asn	Met	Ala	Lys	Leu	545	550	555
Arg	Glu	Arg	Leu	Lys	Gln	Arg	Gln	Gln	Leu	Phe	Asp	Ser	Gln	Gln	560	565	570
Gly	Trp	Phe	Glu	Gly	Trp	Phe	Asn	Lys	Ser	Pro	Trp	Phe	Thr	Thr	575	580	585
Leu	Ile	Ser	Ser	Ile	Met	Gly	Pro	Leu	Leu	Ile	Leu	Leu	Leu	Ile	590	595	600
Leu	Leu	Phe	Gly	Pro	Cys	Ile	Leu	Asn	Arg	Leu	Val	Gln	Phe	Val	605	610	615
Lys	Asp	Axg	Ile	Ser	Val	Val	Gln	Ala	Leu	Ile	Leu	Thr	Gln	Gln	620	625	630
Tyr	Gln	Gln	Ile	Lys	Gln	Tyr	Asp	Pro	Asp	Arg	Pro				635	640	